



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 4, 2022 – 08:28 PM EDT

PDB ID : 5K82
Title : Crystal Structure of a Primate APOBEC3G N-Terminal Domain
Authors : Xiao, X.; Li, S.-X.; Yang, H.; Chen, X.S.
Deposited on : 2016-05-27
Resolution : 2.91 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6342 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G, Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1579	1029	275	265	10			
1	B	188	Total	C	N	O	S	0	0	0
			1578	1029	275	264	10			
1	C	188	Total	C	N	O	S	0	0	0
			1578	1029	275	264	10			
1	D	191	Total	C	N	O	S	0	0	0
			1603	1045	279	268	11			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP M1GSK9
A	-3	PRO	-	expression tag	UNP M1GSK9
A	-2	ALA	-	expression tag	UNP M1GSK9
A	-1	GLY	-	expression tag	UNP M1GSK9
A	0	SER	-	expression tag	UNP M1GSK9
A	143	ALA	-	linker	UNP M1GSK9
A	144	GLU	-	linker	UNP M1GSK9
A	145	ALA	-	linker	UNP M1GSK9
A	146	GLY	-	linker	UNP M1GSK9
B	-4	GLY	-	expression tag	UNP M1GSK9
B	-3	PRO	-	expression tag	UNP M1GSK9
B	-2	ALA	-	expression tag	UNP M1GSK9
B	-1	GLY	-	expression tag	UNP M1GSK9
B	0	SER	-	expression tag	UNP M1GSK9
B	143	ALA	-	linker	UNP M1GSK9
B	144	GLU	-	linker	UNP M1GSK9
B	145	ALA	-	linker	UNP M1GSK9
B	146	GLY	-	linker	UNP M1GSK9
C	-4	GLY	-	expression tag	UNP M1GSK9
C	-3	PRO	-	expression tag	UNP M1GSK9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	ALA	-	expression tag	UNP M1GSK9
C	-1	GLY	-	expression tag	UNP M1GSK9
C	0	SER	-	expression tag	UNP M1GSK9
C	143	ALA	-	linker	UNP M1GSK9
C	144	GLU	-	linker	UNP M1GSK9
C	145	ALA	-	linker	UNP M1GSK9
C	146	GLY	-	linker	UNP M1GSK9
D	-4	GLY	-	expression tag	UNP M1GSK9
D	-3	PRO	-	expression tag	UNP M1GSK9
D	-2	ALA	-	expression tag	UNP M1GSK9
D	-1	GLY	-	expression tag	UNP M1GSK9
D	0	SER	-	expression tag	UNP M1GSK9
D	143	ALA	-	linker	UNP M1GSK9
D	144	GLU	-	linker	UNP M1GSK9
D	145	ALA	-	linker	UNP M1GSK9
D	146	GLY	-	linker	UNP M1GSK9

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	152.40Å 152.40Å 79.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.30 – 2.91	Depositor
% Data completeness (in resolution range)	98.4 (42.30-2.91)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.224 , 0.251	Depositor
Wilson B-factor (Å ²)	69.0	Xtriage
Anisotropy	0.827	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l 0.477 for h,-h-k,-l 0.028 for -k,-h,-l	Xtriage
Total number of atoms	6342	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.